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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,982

DATE: 07/30/2001

TIME: 12:32:42

Input Set : N:\Crf3\RULE60\09757982.txt

Output Set: N:\CRF3\07302001\I757982.raw

3 <110> APPLICANT: Acton, Susan
 5 <120> TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
 7 <130> FILE REFERENCE: MNI-050
 9 <140> CURRENT APPLICATION NUMBER: 09/757,982
 10 <141> CURRENT FILING DATE: 2001-01-10
 12 <150> PRIOR APPLICATION NUMBER: 09/163,115
 13 <151> PRIOR FILING DATE: 1998-09-29
 16 <160> NUMBER OF SEQ ID NOS: 15
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 4137
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: 'n' at positions 2872, 3597 and 3682 may be any nucleic acid
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (297)..(1202)
 32 <400> SEQUENCE: 1
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 35 actccggacg cgcctgcag tgcgcagggt ggggtgcccc cgctgcagc gtccgcggg 120
 37 gcggcgcggc gggagggtgc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180
 39 cgcgctttcc gacggcggcg ccgcgccgag ccacccgccc gcccaaggtc tctcgcgggc 240
 41 gggagaacgg aaaactccca acttcctgag ttctaaagtt cctgttgctt cagaca atg 299
 42 Met
 43 1
 45 gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347
 46 Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
 47 5 10 15
 49 cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395
 50 Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
 51 20 25 30
 53 ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443
 54 Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
 55 35 40 45
 57 aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491
 58 Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
 59 50 55 60 65
 61 cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539
 62 Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys
 63 70 75 80
 65 gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat 587
 66 Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr
 67 85 90 95
 69 tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta 635
 70 Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu
 71 100 105 110

ENTERED

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74 Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln
75      115      120      125
77 aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt 731
78 Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu
79 130      135      140      145
81 tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat 779
82 Cys Ser Ala Leu His Met His Ser Arg Arg Val Met His Arg Asp
83      150      155      160
85 ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt 827
86 Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu
87      165      170      175
89 gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca 875
90 Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala
91      180      185      190
93 cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat 923
94 His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
95      195      200      205
97 gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta 971
98 Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
99 210      215      220      225
101 cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg 1019
102 Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
103      230      235      240
105 aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca cct 1067
106 Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
107      245      250      255
109 ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat atg 1115
110 Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met
111      260      265      270
113 tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt tat 1163
114 Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr
115      275      280      285
117 gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca 1212
118 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
119 290      295      300
121 agatcatgaa gagtgaacc aaagtaattg aaagtatttt gtgcaaagtc gtacctscoc 1272
123 atttatgtct ggggtgtaag attaataatt cagagctagt gtgctctgaa tccttaacca 1332
125 gttttcatat aagcttcatt ttgtaccagt cacctaaatc acctccttgc aacccccaaa 1392
127 tgactttgga ataactgaat tgcatgtag gagagaaaat gaaacatgat ggttttgaat 1452
129 ggctaaaggt ttatagaatt tcttacagtt ttctgctgat aaattgtgtt tagatagact 1512
131 gtcagtgcc aatattgaag gtgcagcttg gcacacatca gaatagactc atacctgaga 1572
133 aaaagtatct gaacatgtga cttgtttctt ttttagtaat ttatggacat tgagatgaac 1632
135 acaattgtga acttttgtga agattttatt tttaaacggt tgaagtacta gttttagtgc 1692
137 ttagcagagt agttttcaaa tatgattcct atgataaatg tagacacaaa ctatttgaga 1752
139 aacatttaga actcttagct tatacattca aaatgtaact attaaatgtg aagatttggg 1812
141 gacaaaatgt gagtcagaca ctgaagagtt ttttgttttg ttttaatat tttgatattc 1872
143 tctttgcatt gaaatggtat aaatgaatcc atttaaaaag tggttaagga tttgttttagc 1932
145 tgggtgtgata ataattttta aagttgcaca ttgcccaagg ctttttttgt gtgtttttat 1992

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147 tgttgtttgt acatttgaaa aatattcttt gaataacctt gcagtactat atttcaagrt 2052
149 ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112
151 ttttattcat aagttttatt gaagttctga tccgtccctt tcagaaattt ttttatatta 2172
153 ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatat 2232
155 tttctgagag tataataccc ttttaaaaga tatttggtat accaataactt ttcctggatt 2292
157 gaaaactttt tttaaacttt ttaaaatttg ggccactctg tatgcatatg tttggctctg 2352
159 ttaaagagga agaaaggatg tgtgttatac tgtacctgtg aatgttgata cagttacaat 2412
161 ttatttgaca aggttgtaat tctagaatat gcttaataaa atgaaaactg gccatgacta 2472
163 cagccagaac tgttatgaga ttaacatttc tattgagaag cttttgagta aagtactgta 2532
165 tttgttcatg aagatgactg agatggtaac acttcgtgta gcttaaggaa atgggcagaa 2592
167 tttcgtaaat gctgttgtgc agatgtgttt tccctgaatg ctttcgtatt agtggcgacc 2652
169 agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtta aaggactctg 2712
171 tgccatctta caaccttgga tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772
173 cacttccctt tagccgatgt aactgctggt tttgtttttc atatgtgttt ttcttacct 2832
W--> 175 catttgaatg ctttcaagca tttgtaaact taaaaaaan wawaaagggc aaaaagtctg 2892
177 aaccttggtt ttctgaaatc taatcagtta tgtatggttt ctgaagggtg attttatttt 2952
179 ggaataggtg aagcgaaacc tgttttgcw tgtttttcct gagggctaga tgcatttttt 3012
181 ttctcacact cttaatgact ttaacattt atactgagca tccatagata tattcctaga 3072
183 agtatgagaa gaattattct tattgacct taatgtcatg ttcattttta tgtaataata 3132
185 ttgagatgaa atgttctctg gttggaacag atactctctt tttttttctt gcaatcttta 3192
187 agaatacata gatctaaaat tcattagctt gaccctcaa agtaactttt aagtaaagat 3252
189 taaagctttt ctctcagtg aatatactg ctagaaggaa atagctggga agaatttaat 3312
191 gatcagggaa attcattatt tctatatgtg gaaacttttt gcttcgaata ttgtatcttt 3372
193 ttaaactctaa atgttcatat ttttctgaa gaaacctg tgtaaaaatc aaattttaat 3432
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197 acctataaaa tgttctttat atgtgttcat aagtaaaatt tatattgatt aagttaaact 3552
W--> 199 tttgaattga tttgaggagc agtaaaatga aagctatatc tattnctaaa ccytatttag 3612
201 acattgkac cagttaccca ggtgaaaata kggagtaact ttgttttgta tggtaagggt 3672
W--> 203 taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732
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209 gatattttatt ttaacaaaaa tgttactcac attaaatgtt tattctttta aatgaatgta 3912
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215 gatttctgtt attagctttg aaaattgtat aatatcctaa tataacaaaa atataaaaaat 4092
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221 <211> LENGTH: 302
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 2
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227 1 5 10 15
229 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
230 20 25 30
232 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
233 35 40 45
235 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
236 50 55 60

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238 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
239 65 70 75 80
241 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
242 85 90 95
244 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
245 100 105 110
247 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
248 115 120 125
250 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
251 130 135 140
253 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
254 145 150 155 160
256 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
257 165 170 175
259 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
260 180 185 190
262 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
263 195 200 205
265 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
266 210 215 220
268 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
269 225 230 235 240
271 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
272 245 250 255
274 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
275 260 265 270
277 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
278 275 280 285
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281 290 295 300
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285 <211> LENGTH: 906
286 <212> TYPE: DNA
287 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (1)..(906)
293 <400> SEQUENCE: 3
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296 1 5 10 15
298 caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96
299 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
300 20 25 30
302 aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144
303 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
304 35 40 45
306 tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa 192
307 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys

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308      50      55      60
310 gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc 240
311 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
312 65      70      75      80
314 aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa 288
315 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
316      85      90      95
318 tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa 336
319 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
320      100      105      110
322 cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag 384
323 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
324      115      120      125
326 caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag 432
327 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
328      130      135      140
330 ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga 480
331 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
332 145      150      155      160
334 gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa 528
335 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
336      165      170      175
338 ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct 576
339 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
340      180      185      190
342 gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata 624
343 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
344      195      200      205
346 cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt 672
347 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
348      210      215      220
350 cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa 720
351 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
352 225      230      235      240
354 atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca 768
355 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
356      245      250      255
358 cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat 816
359 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
360      260      265      270
362 atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt 864
363 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
364      275      280      285
366 tat gac gta gca aag agg atg cat gca tgc act gca agc agc 906
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368      290      295      300
371 <210> SEQ ID NO: 4
372 <211> LENGTH: 2120
373 <212> TYPE: DNA

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VERIFICATION SUMMARY

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L:199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1